

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently Amended) A crystal of a polypeptide ~~having~~ consisting of the amino acid sequence of residues 29-766 of SEQ ID NO: 2 and a polyhistidine tag optionally being added to a C-terminal side or N-terminal side thereof wherein the crystal has a space group of $P2_12_12_1$ and diffracts x-rays for the determination of the atomic coordinates of the polypeptide at a resolution of 3 Å or less.
2. (Cancelled)
3. (Currently Amended) A crystal of a polypeptide ~~having~~ consisting of the amino acid sequence of residues 33-766 of SEQ ID NO: 2 and a polyhistidine tag optionally being added to a C-terminal side or N-terminal side thereof wherein the crystal has a space group of $P2_12_12_1$ and diffracts x-rays for the determination of the atomic coordinates of the polypeptide at a resolution of 3 Å or less.
4. (Currently Amended) The crystal according to claim 1 or 3 wherein the crystal ~~has a space group of $P2_12_12_1$, and~~ a lattice constant of the unit cell of $|a| = 118.0 \pm 5.0\text{Å}$, $|b| = 125.9 \pm 5.0\text{Å}$, $|c| = 136.8 \pm 5.0\text{Å}$, and $\alpha = \beta = \gamma = 90^\circ$, and is orthorhombic.
5. (Previously Presented) The crystal according to claim 1 or 3 wherein the crystal has the structural coordinates shown in Figure 4.
6. (Previously Presented) The crystal according to claim 1 or 3 wherein the crystal has structural coordinates different from the structural coordinates as shown in Figure 4 via fluctuation of a protein.

7-24. (Cancelled)

25. (Previously Presented) The crystal according to claim 1 or 3, wherein the polyhistidine tag is added to the C-terminal side of the polypeptide.

26. (Previously Presented) The crystal according to claim 1 or 3 wherein the crystal diffracts x-rays for the determination of the atomic coordinates of the polypeptide at a resolution of 2.8 Å or less.

27. (Previously Presented) The crystal according to claim 1 or 3 wherein the crystal diffracts x-rays for the determination of the atomic coordinates of the polypeptide at a resolution of 2.6 Å or less.

28. (Previously Presented) The crystal according to claim 1 or 3, wherein amino acid residues Ser 630, Asp 708 and His 740 of SEQ ID NO:2 have the structural coordinates shown in Figure 4.